

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2002, 08:42:08 ; Search time 223.75 Seconds
(without alignments)
254.911 Million cell updates/sec

Title: US-08-212-185-12

Perfect score: 770

Sequence: 1 MAQNQLQQLDRLYLKQLHQ.....QFESLTFDMLTSECATSPM 770

Scoring table:

Gapop 60.0 , Gapext 60.0

Search:d: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_1101.*

1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	770	16	Mouse Stat3 (19sf6
2	770	100.0	770	17	Mouse STAT4, Mus
3	568	73.8	770	21	N-terminal domain
4	532	69.1	770	20	Human STAT3 allele
5	532	69.1	793	21	Lung cancer associ
6	442	57.4	770	16	Mouse liver acute
7	393	51.0	393	22	Mouse Stat3 protei
8	271	35.2	271	22	Mouse Stat3 protei
9	252	32.7	252	22	Mouse Stat3 protei
10	236	30.6	236	22	Mouse Stat3 protei
11	229	29.7	229	22	Mouse Stat3 protei

12	223	29.0	223	22	AA72854	Mouse Stat3 protei
13	221	28.7	770	16	AA82993	Human placenta acu
14	221	28.7	770	22	AA819964	Human signal trans
15	213	27.7	213	22	AA72851	Mouse Stat3 protei
16	210	27.3	229	22	AA72862	Mouse Stat3 protei
17	207	26.9	228	22	AA72861	Mouse Stat3 mutant
18	207	26.9	229	22	AA72863	Mouse Stat3 mutant
19	194	25.2	229	22	AA72860	Mouse Stat3 protei
20	185	24.0	185	22	AA72855	Mouse Stat3 protei
21	176	22.9	176	22	AA72848	Mouse Stat3 protei
22	154	20.0	154	22	AA72840	Mouse Stat3 protei
23	143	18.6	143	22	AA72849	Mouse Stat3 protei
24	141	18.3	141	20	AA707240	Fragment of human
25	139	18.1	173	22	AA819973	Human STAT-3 DNA b
26	138	17.9	141	20	AA707241	Fragment of mouse
27	129	16.8	129	22	AA72856	Mouse Stat3 protei
28	128	16.6	128	22	AA72852	Mouse Stat3 protei
29	112	14.5	112	17	AAW03167	Mouse STAT4 DNA bi
30	103	13.4	141	20	AAW07239	Fragment of human
31	96	12.5	96	22	AA72857	Mouse Stat3 protei
32	95	12.3	95	22	AA72853	Mouse Stat3 protei
33	22	2.9	22	22	AA73232	Stat3 SH2 domain C
34	14	1.8	14	21	AA812847	STAT3 tyrosine pho
35	12	1.6	12	17	AA898426	STAT3 peptide, Ser
36	12	1.6	107	22	AA819971	Human STAT-1 SH2 d
37	12	1.6	376	22	AA72845	Mouse Stat1 protei
38	12	1.6	582	19	AAW62996	Human truncated St
39	12	1.6	701	14	AA841335	84 kD ISGF-3alpha.
40	12	1.6	712	16	AA72079	Human Stat84, Hom
41	12	1.6	712	17	AAW03170	Human STAT1-beta.
42	12	1.6	712	19	AAW62995	Human Stat1-beta p
43	12	1.6	739	14	AA841334	91 kD ISGF-3alpha.
44	12	1.6	749	16	AA72080	Mouse Stat1 (Stat9
45	12	1.6	749	17	AAW03172	Mouse STAT1, Mus

ALIGNMENTS

RESULT 1
AA72082
ID AAR72082 standard; Protein; 770 AA.
XX
AC AAR72082;
XX
DT 27-SEP-1995 (first entry)
XX
DE Mouse Stat3 (19sf6).
XX
KW Signal transducer and activator of transcription; STAT; 19sf6;
KW Stat3; receptor recognition factor; transcription factor;
KW cellular debilitation; derangement; dysfunction;
KW interferon-gamma.
XX
OS Mus sp.
XX
PN WO9508629-A.
XX
PD 30-MAR-1995
XX
PF 26-SEP-1994; 94WO-US10849.
XX
PR 24-SEP-1993; 93US-0126588.
PR 24-SEP-1993; 93US-0126595.
PR 11-MAR-1994; 94US-0212184.
PR 11-MAR-1994; 94US-0212185.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Darnell JE, Schindler CW, Shuai K, Wen Z, Zhong Z;
XX WPI: 1995-139598/18.
DR N-PSDB; AAQ89340.

XX	Receptor recognition factor implicated in transcriptional stimulation of genes - useful in drug screening assays and/or for treating cellular debilitations, derangements and/or dysfunctions, etc.	
PT	Claim 1; Page 107-110; 160pp; English.	
PS		
XX		
CC	A fragment encoding the human Stat91 protein was used to screen a murine thymus and spleen cDNA for homologous proteins. A highly homologous gene (given in AA089338) was isolated that encoded a 91 kDa protein (AAR72080) (Stat1) that was responsive to interferon-gamma. Using a fragment of the mouse gene as probe, 2 additional members of the 113-91 family of receptor recognition factor proteins were isolated. The 2 genes (AA089339-40) were cloned in plasmids 13sfl and 19sf6 and encoded proteins termed Stat4 (AAR72081) and Stat3 (AAR72082), respectively.	
XX	Sequence 770 AA;	
SQ		
Query Match	100.0%; Score 770; DB 16; Length 770;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 770; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 MAQWNLQQLDTRYLKQLHOLYSDTFPEMELROFLAPWIESODWAYAASKESHATLVFHNL 60	
Db	1 maqwnqlqldtrylkqlhlysdtfpmlrqlflapwiesqdwayaaskeshatlvfhn1 60	
Oy	61 LGEIDDOQYSRFLQESNVLYQHNLRRIRKOFLOSRYLEKPMELRIARIVARCLWEESRLLOTA 120	
Db	61 lgeidqqysrflqesnvlyqhnrrirkflqsrlylekpmeiarivarclweesrl1lqtaa 120	
Oy	121 TAAQGGGANHPTAAVTEKQOMLEQHLQDVRRKRVQDLQKMKVVENLQDDDFDNFKYTLK 180	
Db	121 taadqggqanhpptaavtekgqlqhlqdvrvkrvqdlqgmkvvenlqddfdfnkylk 180	
Oy	181 SQGDMQDLGNQNSVTRQKMOQLTALDOMRRSTVSELAGLLSAMXYVQKTLTDEEL 240	
Db	181 sqgdmqdlngnnsqvtrqkmoqltaldomrrstvselagllsamxyvqkltdeel 240	
Oy	241 ADWRRRPIACIGPPNICDLRLENWITSLSAESQLOTRQOIKLEELQKVSYGDPVQ 300	
Db	241 adwrrrpiaci9ppnicdlrlenwitslaesqltrqgikkleelqgkvsykgdpivq 300	
Oy	301 HRPMLERIVELFNLAKSAFVVERQPCMPHDPRLVIKTCYQFTTKVRLLYKFPPELNY 360	
Db	301 hrpmlerivelfnlmksafvverqpcmpmpdprrlviktqvgftckvrllykfpelny 360	
Oy	361 QLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAFFKHLTLREORCGN 420	
Db	361 qlkikvcidksgdvaalrgsrkfnlgtntkvmnmeesnngslsaefkhltlreorcgn 420	
Oy	421 GGRANCASLIIVTEELHLITFEVYHOGUJLKDLETHSLPWWVISNTQCPNNAWA:ILWY 480	
Db	421 ggrancasliivteelhlitfevyhqqikidletshslpwwvisnqcpnawasilwy 480	
Oy	481 NMLTNNPKNVNFFTKPPIGTWQDAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540	
Db	481 nmltnnpkvnfftkppigtwdqvaevlswqfssttkrglsieqlttlaekllpggvnys 540	
Oy	541 GCQITWAKFCCKENMAGKGFSSFWNLDMIIDLVKKYILALWNEGYIMGFISKERERAILST 600	
Db	541 gcqitwakfckenmagkgfswwldnldlvkkyilalwnegyimgfiskerailst 600	
Oy	601 KPGCTFLLRFSRSKEGCVFTTWKEDISCKTOIQSVEPYTKKOOLNNMSPAEIIMGYKIM 660	
Db	601 kpgctflirfseskegcvfttwekdisgktqlqsvepytkqqlnmsfaeiimgykim 660	
Oy	661 DATNILVSPVLVLPDIPKEAFGKYCRPESQEPHADPGSAAPYLTKFTICVPTPTCSN 720	
Db	661 datnilvspvlvlpdipkeafgkycrpesqepheadpgsaapy1ktkfticvptptcsn 720	

Oy	721 TIDPMSPTLDSLMOFGNNGEAGPESAGGOFESLTFDMDLTSECATSPM 770	
Db	721 tidpmsprtldslmqfgnnggeagsaggqfesi1fdmdltsecatspm 770	
RESULT 2		
AAW03176		
ID	AAW03176 standard; Protein; 770 AA.	
XX		
AC	AAW03176;	
XX		
DT	24-OCT-1996 (first entry)	
XX		
DE	Mouse STAT4.	
XX		
KW	STAT4; signal transducer and activator of transcription;	
KW	DNA binding protein; ligand; receptor; oncogenesis; inflammation;	
XX	autoimmune disease; antagonist; therapy.	
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	Domain	398..508
FT		/label= DNA_binding_domain
FT		/note= "Claim 3, page 110"
XX		
PN	W09620954-A2.	
XX		
PD	11-JUL-1996.	
XX		
PF	28-DEC-1995; 95WO-US17025.	
XX		
PR	06-JAN-1995; 95US-0369796.	
XX		
PA	(UYRQ) UNIV ROCKEFELLER.	
XX		
PI	Darnell JE, Horvath CM, Wen Z, Zhong Z;	
XX		
DR	WPI: 1996-333941/33.	
DR	N-PSDB: AAT31280.	
XX		
PT	New STAT protein DNA-binding domain peptide(s) - useful for	
PT	diagnosing, preventing or treating cellular dysfunction, e.g.	
PT	oncogenesis, inflammation, parasitic disease or autoimmunity	
XX		
PS	Disclosur-; Page 87-90; 138pp; English.	
XX		
CC	Mouse signal transducer and activator of transcription (STAT)	
CC	protein STAT4 (AAW03176) serves a dual purpose, i.e. signal	
CC	transduction from ligand-activated receptor kinase complexes	
CC	followed by nuclear translocation and DNA binding to activate	
CC	transcription. Recombinant STAT4 can be obt'd. using cDNA clone	
CC	19sf6 (AAT31278) obt'd. from splenic/thymic cells. STAT4 includes	
CC	a DNA-binding domain (see also AAW03167) capable of both	
CC	receptor recognition and message delivery via DNA binding in a	
CC	receptor-ligand specific manner. STAT proteins and their DNA	
CC	binding domains (see also AAW03165-75) are useful for screening	
CC	antagonists used to inhibit STAT-mediated signal transduction	
CC	and activation of transcription.	
XX		
SQ	Sequence 770 AA;	
Query Match	100.0%; Score 770; DB 17; Length 770;	
Best Local Similarity	100.0%; Pred. No. 0;	
Matches 770; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 MAQWNLQQLDTRYLKQLHOLYSDTFPEMELROFLAPWIESODWAYAASKESHATLVFHNL 60	
Db	1 maqwnqlqldtrylkqlhlysdtfpmlrqlflapwiesqdwayaaskeshatlvfhn1 60	
Oy	61 LGEIDDOQYSRFLQESNVLYQHNLRRIRKOFLOSRYLEKPMELRIARIVARCLWEESRLLOTA 120	

Db	61	lgeidqgysrflqesnvlyqghnlrrrikfqlgsrylekpmeariavarcrlweesrltqaa	120
QY	121	TAAQGGQANHPHTAAVVTKEQOMLEQHLQDYKRKYODLEQKMKVVENLQDDFQNFYKTLK	180
Db	121	taaqggqanhtaavvtkekqmqleqhlqdvkrvqdeqkmkveenlqdddfnfyktlk	180
QY	181	SQGDMDLNGNNSVTRQKMQOQLFQMLTALDOMRRSIVSELAGLLSAMEYVQKLTDEEL	240
Db	181	sggdmqdlngnqsvtrqkmdqlqemltaldqmrslvselagllsameyvvqkltldeei	240
QY	241	ADWKRPRPIACTIGPPNICIDLRLENWJTSLAESOLOTRQOIKKLEELQKQSVKGDPIVO	300
Db	241	adwkrprpeiacigppnicidlrlewnitslaesqlqtrqqikleelqkvsvkgdipi	300
QY	301	HRPMLERIVELFRLNLMKSAFVWRQPCMPHPDRPLVIKTGYQFTTKVRLVLVKFPELNY	360
Db	301	hrpmlleerivelfrlnlmsafvwrqpcmpmhprplviktgvqfttkvrlvlvkfpelny	360
QY	361	QLKIKVCIDKDSGDAALRGSRKFNLITGNTKVMNNEESNNGSLSAFFKHLTLRQRCGN	420
Db	361	qlkikvcidkdsdvaalrgsrkfnlgtntkvmnneesnngslsaefkhltilreqrcgn	420
QY	421	GGRANCASLIIVTEELHLITFETEVYHGLKIDLETHSLPVPVVISNICOMPNAWASILWY	480
Db	421	ggrancdasliivteelhlitfetevyhglkidlETHslpvvvisnicompnawasilwy	480
QY	481	NMLTNPNKNVNFYTKPPIGTWDQVAEVLWSQFSTTKRGLSTEQLTTLAEKLLGPGVNVYS	540
Db	481	nmltnpknvnfytckpplgtwdqvaevlswqfsttkrglsieqltlaekllpgvnyys	540
QY	541	GCQITWAKFCENMAGKGFSPFWMLDNIIDLVKYILALWNEGYIMGFISKERERAILST	600
Db	541	gcqitwakfcenmagkgfswwwwldniidlvkylalwnegyimgfiskereraillst	600
QY	601	KPPGTFLRLRSESKEGCVTFTWVEKDICKTOIQSVPEYTKQOLNNMSFAEIIIMGYKIM	660
Db	601	kppdtflrlrseskeggvftwvekdiskgtkqsvpeytkqolnnmsfaeiiimgykim	660
QY	661	DATNILVSPVLVYPDIPKPEAFGKCYRPEQSEHPHADPGSAAPYLKTKFCVTPTTTCGN	720
Db	661	datnilvspvlvypdipkpea fgykrpesqehpeadpgsaapylktkfcvtpttcsn	720
QY	721	TIDIPMSPTRLDSLMQFGNNGEAGPFSAGQGFESLTFDMDLTSECATSPM	770
Db	721	tidi pmsprtldslmqfgngeagpfsagqgfesltfdmdltsecatspm	770
RESULT	3		
AAAB12377			
ID	AAAB12377	standard; peptide; 770 AA.	
XX	AAAB12377:		
XX	AC		
XX	DT	08-NOV-2000 (first entry)	
XX	DE	N-terminal domain of murine STAT-3 protein.	
XX	DE		
KW	STAT; signal transducer and activator of transcription; crystal:		
KW	drug design; murine.		
XX	OS	Mus sp.	
XX	XX		
FT	Key	Location/Qualifiers	
FT	Region	4..9	
FT	FT	/Label= "Alpha helix 1"	
FT	FT	12..21	
FT	FT	/Label= "Alpha helix 2"	
FT	FT	19..21	
FT	FT	/Label= "3(10) helix of alpha helix 2"	
FT	FT	28..33	
FT	FT	/Label= "Alpha helix 3"	
FT	FT	35..40	
FT	FT	/Label= "Alpha helix 4"	

Db 361 qlkikvcidkugdvaaigrskkniltgntkvmmeesnnngsisaefkhlitlreqrcgn 420
Qy 421 GGRANCASLIVTEELHLITETETEVYHGLKTDLETHSLPVVVVISNICOMPNAWASILWY 480
Db 421 ggrancdaslivteehlitetevyhgldkldlethslpvvvvisnicompnaasilwy 480
Qy 481 NMLTNPKNVNFTKPPICCTWDQVAEVLWQFSSTTKRGLSTIEQITTLAEKLLGPGVWVS 540
Db 481 nmltnpnknvnftkppigtwdqvaevlswqfssttkrglsieqittlaekllgpgvnys 540
Qy 541 GCOITWAKFCKENACKGFSFWWLDNIIDLKYLALWNEGYIMGFTSKRERAILST 600
Db 541 gcqitwakfckenackgfsfwwldnildlvkylalwnegyimgfiskereraillst 600
Qy 601 KPPCTELLRFSSSESGGVYFTWVEKDISGKTQIOSVEPYTKQOLNNMSFAEILINGYKIM 660
Db 601 kppgtellrfsssesggvftcwekdlsqktqigsvepytkqolnnmsfaelingykim 660
Qy 661 DATNILVSLVLYLPDIKPEEAFGYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720
Db 661 datnilvslvlylpdikpeeafgycrpesqehpeadpgsaapyiktkfvcvtpttcsn 720
Qy 721 TIDLPMSPRTLDSLMQFGNNGGAEPGAGQGFESLTFDMDLTSECATSPM 770
Db 721 tidlpmsprtlslmqfgnnggaepsagqgfesltfdmdltsecatspm 770
RESULT 4
AAV03768
ID AAV03768 standard; Protein; 770 AA.
XX AC AAV03768;
XX DT 11-JUN-1999 (first entry)
XX DE Human STAT3 allelic variant.
XX KW Signal Transducer and Activator of Transcription 3; STAT3; allele; IL-6;
KW intracellular transcription factor; interleukin-6; medicament; variant;
KW pharmaceutical; autoimmune disease; inflammatory; human.
XX OS Homo sapiens.
XX PN EP905234-A2.
XX PD 31-MAR-1999.
XX PF 18-FEB-1998; 98EP-0102774.
XX PR 16-SEP-1997; 97EP-0116061.
XX PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PI Della Pietra L, Serlupi-Crescenzi O;
XX WPI; 1999-192664/17.
XX N-PSDB; AAX29281.
XX PT New human Signal Transducer and Activator of Transcription 3 (STAT3)
XX allelic variant useful for treatment of autoimmune and inflammatory
XX disease
XX PS Claim 2; Page 9-13; 32pp; English.
XX CC The present sequence represents a predominant allelic variant of human
XX Signal Transducer and Activator of Transcription 3 (STAT3) protein, an
XX intracellular transcription factor which mediates IL-6 signals. The
XX encoding sequence differs from the original published human STAT3 gene
XX sequence (Akira et al., 1994). Host cells comprising a recombinant STAT3
XX DNA molecule can be used for the recombinant expression of the variant.
XX STAT3 protein is useful as a medicament or pharmaceutical composition for
XX treatment of autoimmune or inflammatory diseases.

SQ Sequence 770 AA;
Query Match 69.1%; Score 532; DB 20; Length 770;
Best Local Similarity 59.7%; Pred. No. 0;
Matches 732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 26 FPMELRQFLAPWIESODMAYAAKESHATLVFHNLLIGLIDQOYSRFLQESNVLVYOHNLRR 85
Db 26 fpmelrqflapwiesodmayaaakeshatlvfhnlligldqoysrflqesnvlvghnlrr 85
Qy 86 IKQFLQSRYLEKPEMEIARIVARCLWEESRLLOTAATAAQCGQGANHPTAAVVTKEQOMLE 145
Db 86 ikqflqsrylekpemeiarivarcliweesrllqtaataaqqggqganhptaavvtekkqgle 145
Qy 146 QHLQDVVF KVQDLEQKMKVVENLQDDFDENYKTLKSGQMDQDLNNGNOSVTRQKMQOLEQ 205
Db 146 qhlqdvrvkvdleqkmkvvenlqddfdenfnyktlksqgmdqdlngnngsvtrqkmqleq 205
Qy 206 MLTALDOMRRSIVSEIAGILSAMEYVQKTLTDEELADWKKRPEIACIGGPPNICLDRIEN 265
Db 206 mltaldomrrsivselagilsameyvvqkltldeeladwkrqgiacigppnicldrien 265
Qy 266 WITSIAESQLOTRQOIKKLEELQOAKVSKGDPVQHRPMLPERIVELFRNLKMSAFVVER 325
Db 266 witsiaesqltrqoikkleelqoakvskgdpivqhrpmlperivelfrnlkmsafvver 325
Qy 326 OPCMPMPDRPLVIKTVGFQFTKVRLLVKFPPELNTQLKIKVCIDKDSGDVAALRGRKFN 385
Db 326 opcmpphdpdrplviktvqfctkvrllvkfpeelnqyqlkikvcidkdsgdvaalrgrkfn 385
Qy 386 ILGTNTKVMNEESNNGSLSAEFKHLITLREQRCGNGGRANCDASLIVTEELHLITFETEV 445
Db 386 ilgtntkvmneesnngslsaefkhlitlreqrcgnggrancdaslivteelhlitfetev 445
Qy 446 YHGLKIDLETHTSLPVVVISNICOMPNAWASILWYNMLTNPNKNVNFYTKPPIGTWDQVA 505
Db 446 yhgldkldlethslpvvvvisnicompnawasilwynmltnpnknvnftckppigtwdqva 505
Qy 506 EVLSWQFSSTTKRGLSIEQITTLAEKLLGPGVNYSCQITWAKFCKENACKGFSFWWVL 565
Db 506 evlswqfssttkrglsieqittlaekllgpgvnysqcitwakfckenackgfsfwvl 565
Qy 566 DNIIDLKVKYILALWNEGYIMGFTSKRERAILSTKPPGFTLLRFSESSREGCVTTTWE 625
Db 566 dniidlvkylalwnegyimgfiskereraillstppgftllrfsseskeggvtttwe 625
Qy 626 KDISGKTQIOSVEPYTKQOLNNMSFAEIIMGYKIMDATNILVSPLYLYLPDIKPEEAFGK 685
Db 626 kdisgktqigsvepytkqolnnmsfaeiimgykimdtnilvslplylylpdikpeeafigk 685
Qy 686 YCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGGAEE 745
Db 686 ycrpesqehpeadpgsaapyiktkfvcvtpttcsntidlpmsprtlslmqfgnnggae 745
Qy 746 PSAGGQFESLTFDM 759
Db 746 psaggqfesltfdm 759
RESULT 5
AAB58442
ID AAB58442 standard; Protein; 793 AA.
XX AC AAB58442;
XX DT 14-MAR-2001 (first entry)
XX DE Lung cancer associated polypeptide sequence SEQ ID 780.
XX KW Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antineoplastic; gynecological;

CC from a mouse liver cDNA library using a polymerase chain reaction
CC product (amplified using primers derived from an IL-6-treated mouse
CC liver peptide) as a probe. APRF-inhibitors, e.g. antibodies,
CC antisense oligonucleotides or ribozymes, may be used to treat
CC diseases induced by IL-6, e.g. inflammatory disease, leukemia,
CC cancer, osteoclasia, pulmonary hypertension, etc.
XX
SQ Sequence 770 AA:

Query Match 57.4%; Score 442; DB 16; Length 770;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 742; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 26 FPMELROFLAPWIESQWYAYASKESHATILVFHNLGELIDQOYSRFLQESNVLYOHNLR 85
Db 26 fpmelrqflapwiesqdwayaaskeshatlvfhnlgeidqqysrflqesnvlyqhnlr 85
Qy 86 IKFLOSRYLEKPMETARIVARCLWEESRLLOTATAAQQGGQANHPTAAVVTETKQOMLE 145
Db 86 ikfqlsrylekpmetarivarclweesrlqltaataaqqggqanhptaavvtektqomle 145
Qy 146 QHLODVRKRVODLEQKMKVVENIQDDFDENYKTLKSGQDMQDLNGNQSVTRKMQOOLEQ 205
Db 146 qhlqdvrvqgdlqkqmkvveniiddfdnynkylksqgdmqdlngnqvtrqkmgqleq 205
Qy 206 MLTALDOMRESIVSELGALSAMEYVQKTLTDEELADMKRRPEIACIGGPPNICIDRLN 265
Db 206 mltdldmrrsivselaglsameyqkltldeeladmkrrqriaciaggppnicidrln 265
Qy 266 WITSLAESQLOTRQIKKLELOKVSYGDPVIVQHRPMLERIVELFRLNLMKSAFVVER 325
Db 266 witslaesqlotrqikkleelqkvsygdvpivqhrpmleriveifrlnmlksafvver 325
Qy 326 OPCMPMPDRLVKTGVQFTKVRLLKFPPELNYQLKIVCIDKSDGVAALRGSRKFN 385
Db 326 opcmmpdpdrvltkvqftkvrllkfppeelnynqlkivcidksgdvaalrgsrkfn 385
Qy 386 ILGNTKVMNMEESNNGSLAEFKHLTLRQRCNGGRANCDSALIVTELHLITFETEV 445
Db 386 ilgntkvmneesngslsaefkhltlreqrcnggrancdsalivteelhlitfetev 445
Qy 446 YHOGKLTDLTHSLPVVVISNICOMPNAWAS ILWYNMLTNNPKNVNFTKPPIGTWDOVA 505
Db 446 yhogkltldthslpvvvisnicompnawasilwynmltnnpknvnftkppigtwdova 505
Qy 506 EVLSNQFSSTTKRGLSIEQTLTAEKLLGPGVNYSGCQITWAKFCENMAGKGFSPWML 565
Db 506 evlsnqfssttkrglsieqlttlaekllpgvnysgcqltwakfckenmagkgsfwwl 565
Qy 566 DNIIDLKYYLALWNEGYIMGFISKERERAILSTRPPGTFLRFSSKEGGVTTWVE 625
Db 566 dniidlvykylalwnegyimgfiskererailstkppgtflrfsskeggvttwve 625
Qy 626 KDISGKTOIQSVEPYTKQOLNNNSFABIIMGYKIMDATNIVSPLVLYPDIPKEAFGK 685
Db 626 kdisgktoiqsvepytkqolnnnsfabiimgykimdntnllvslvlylpydpkpeafgk 685
Qy 686 YCRPESQHPADPGSAAPYLKTKFICVPTTCSNTIDLPMSPRTLDSLMQFGNNEGAE 745
Db 686 ycrpesqhpdpadpgsaapylktkfcvpttcsntidlpmsprtltdslmqfgnnegae 745
Qy 746 PSAGGQFESLTFDMDLTSECATSPM 770
Db 746 psaggqfessltdfmdltssecatspm 770

RESULT 7
AAV72842
ID AAV72842 standard; protein; 393 AA.
XX
AC AAV72842;
XX

DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #3 (378-770 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US23822.
XX
PR 31-AUG-1999; 99US-0387418.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Barnell JE;
XX
XX WPI; 2001-226705/23.
DR
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
XX
XX Example 2; Page 68-69; 86pp; English.
CC
CC The present sequence is mouse Stat3 protein fragment containing 378-770
CC amino acids of Stat3 protein. This Stat3 fragment showed very weak
CC binding to c-Jun protein in the cell extract.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulate
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX
SQ Sequence 393 AA:

Query Match 51.0%; Score 393; DB 22; Length 393;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 378 LRGRKFNILGNTKVMNMEESNNGSLAEFKHLTLRQRCNGGRANCDSALIVTELH 437
Db 1 lrgrskfnlilgntkvmneesngslsaefkhltlreqrcnggrancdsalivteelh 60
Qy 438 LITFTEVYHOGKLTDLTHSLPVVVISNICOMPNAWAS ILWYNMLTNNPKNVNFTKPP 497
Db 61 litfetevyhqlkldlethslpvvvisnicompnawasilwynmltnnpknvnftkpp 120
Qy 498 ICTWDOQVAEVLWQFSSTTKRGLSIEQTLTAEKLLGPGVNYSGCQITWAKFCENMAGK 557
Db 121 igtwdqvaevlwqfssttkrglsieqlttlaekllpgvnysgcqltwakfckenmagk 180
Qy 558 GFSFWWYLDNIIDLKYYLALWNEGYIMGFISKERERAILSTRPPGTFLRFSSSKEG 617
Db 181 gfsfwvwdniidlvykylalwnegyimgfiskererailstkppgtflrfsseskeg 240
Qy 618 GVTFTWVEKDISGKTOIQSVEPYTKOOLNNNSFAEIMGYKIMDATNIVSPLVLYPDI 677
Db 241 gvtftwekdsgktqigsvepytkqolnnnsfaelimgykimdntnllvslvlylpydi 300
Qy 678 PKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVPTTCSNTIDLPMSPRTLDSLMQF 737
Db 301 pkeefgkycrpesqhpdpadpgsaapylktkfcvpttcsntidlpmsprtltdslmqf 360

transcription e.g., cellular transformation. These identifying agents are used in the treatment of dysproliferative diseases and also for treating cancer and psoriasis. A stat protein comprises the N-terminal domain, coiled-coil domain, DNA binding domain, linker domain, SH2 domain and transactivation domain.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

CC The present sequence is mouse Stat3 protein fragment containing 130-358
CC amino acids of Stat3 protein. This Stat3 fragment showed strong
CC binding to c-Jun protein in the cell extract.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX Sequence 229 AA:
SQ

Query Match 29.7%; Score 229; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 8e-230;
Matches 229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130 NIPTAAVYTEKQMLEQHLQDVRRVQDEQKMKVVENLQDDFDNYKTLKSGQDMQDLN 189
DB 1 NIPTAAVTEKQMLEQHLQDVRRVQDEQKMKVVENLQDDFDNYKTLKSGQDMQDLN 60
QY 190 GNNQSVTRQKMOQLQMI TALDOMRRSTVSELAGLLSAMEYVQKTLTDEELADWKRPEI 249
DB 61 GNNQSVTRQKMQLEQMLTALDQMRISVSELAGILSAMEYVQKTLTDEELADWKRPEI 120
QY 250 ACIGGPPNICLDRLENWITSLAESOLQTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 309
DB 121 ACIGGPPNICLDRLENWITSLAESQLTRQIKKLEELQOKVSYKGDPIVQHRPMLERI 180
QY 310 VELFRNLKSAFVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPEL 358
DB 181 VELFRNLKSAFVERQPCMPHDPRLVIKTVGQFTTKVRLLVKFPPEL 229

RESULT 12
AAY72854
ID AAY72854 standard; protein; 223 AA.
XX
AC AAY72854;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #12 (155-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 188..204
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
XX
XX W0200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US23822.
XX
XX 31-AUG-1999; 99US-0387418.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between

PT transcription factor c-Jun and a Stat3 protein -
XX Claim 65; Page 79; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 155-377
CC amino acids of Stat3 protein.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX Sequence 223 AA:
SQ

Query Match 29.0%; Score 223; DB 22; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.4e-223;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 155 VODLEQKMKVVENLQDDFDNYKTLKSGQDMQDLNNGNNSVTROKMOQLFQMLTALDQMR 214
DB 1 VQDLEQKMKVVENLQDDFDNYKTLKSGQDMQDLNNGNNSVTROKMOQLFQMLTALDQMR 60
QY 215 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLENWITSLAESQ 274
DB 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEIACIGGPPNICLDRLENWITSLAESQ 120
QY 275 LQTRQIKKLEELQOKVSYKGDPIVQHRPMLERIIVELFRNLKSAFVERQPCMPHDP 334
DB 121 LQTRQIKKLEELQOKVSYKGDPIVQHRPMLERIIVELFRNLKSAFVERQPCMPHDP 180
QY 335 RPLVIKTVGQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGVAA 377
DB 181 RPLVIKTVGQFTTKVRLLVKFPPELNYQLKIKVCIDKDSGVAA 223

RESULT 13
AAR82993
ID AAR82993 standard; protein; 770 AA.
XX
AC AAR82993;
XX
DT 25-MAR-1996 (first entry)
XX
DE Human placenta acute phase response factor protein.
XX
KW human; acute phase response factor; transcription factor;
KW interleukin-6; signal transduction; placenta; antibody; antisense;
KW ribozyme; antiinflammatory; antitumor; hypotensive; therapy.
XX
OS Homo sapiens.
XX
XX EP676469-A2.
XX
XX 11-OCT-1995.
XX
XX 29-MAR-1995; 95EP-0104670.
XX
XX 04-APR-1994; 94JP-0065825.
XX
XX (KISH/) KISHIMOTO T.
XX
XX Akira S, Kishimoto T;
XX WPI; 1995-346089/45.
XX N-PSDB; AAT05416.
XX
XX New acute phase response factor - for developing inhibitory agents
XX for treatment of diseases induced by cytokine(s) such as IL-6, e.g.
PT

FT	FT	Region	1..25


```

Query Match      26.9%; Score 207; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 6.5e-207;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 RKRVDLEQKMKVVENLQDDFDNFYKTLKSGDMDLNGNQSVTQRKMQQLLEQMLTALD 211
DB 23 rkrvqdeqkmkvvlenlqddfdnfykltksgdmdlgnngsvtrqkmgqleqmltald 82
QY 212 QMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSIA 271
DB 83 qmrsvselagilameyvqkltldeeadwkrpeiacigppnicldrlenwitsia 142
QY 272 ESOLQTRQOIKKLEELQOKVSKGDPVQHRPMLERIVELFRNLKMSAFVVERQPCMPM 331
DB 143 esqltrqrqkllleelqkvskgdpvqhrpmlerivelfnlmksafvverqpcmpm 202
QY 332 HPDRPLVKTGVQFTTKVRLLLVKFPEL 358
DB 203 hpdprlviktgvqfttkvrlvllvkfpel 229

RESULT 19
AAY72860
ID AAY72860 standard; protein; 229 AA.
XX
AC AAY72860;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 mutant (L148A,V151A,T346A,K348A,R350A) protein fragment.
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy; mutant; muten.
XX
OS Mus musculus.
XX
FH Key
FH Region 1..25
FT /note= "Stat3-c-Jun interaction region 1;
FT corresponds to 130-154 position of Stat3 protein"
FT Misc-difference 19
FT /note= "Wild type Leu substituted with Ala;
FT corresponds to 148 position of Stat-3 protein"
FT Misc-difference 22
FT /note= "Wild type Val substituted with Ala
FT corresponds to 151 position of Stat-3 protein"
FT Region 213..229
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
FT Misc-difference 217
FT /note= "Wild type Thr substituted with Ala
FT corresponds to 346 position of Stat-3 protein"
FT Misc-difference 219
FT /note= "Wild type Lys substituted with Ala
FT corresponds to 348 position of Stat-3 protein"
FT Misc-difference 221
FT /note= "Wild type Arg substituted with Ala
FT corresponds to 350 position of Stat-3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US23822.
XX
XX 31-AUG-1999; 99US-0387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszynska MH, Darnell JE;
PI
```

```

XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein .
XX
XX Example 4: Page -: 86pp; English.
XX
XX The present sequence is mouse Stat3 mutant protein fragment containing
XX 130-358 amino acids of Stat3 protein. This mutant is obtained by
XX replacing Leu 148 with Ala, Val 151 with Ala, Thr 346 with Ala, Lys 348
XX with Ala and Arg 350 with Ala in the Stat3 protein.
XX The invention relates to methods for identifying interacting regions of
XX transcription factors and methods for identifying agents which modulates
XX the interaction between a transcription factor such as c-Jun and a Stat
XX protein such as Stat-1 and Stat-3, useful for modulating gene
XX transcription e.g., cellular transformation. These identifying agents are
XX used in the treatment of dysproliferative diseases and also for treating
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
XX transactivation domain.
XX
XX Sequence 229 AA:

Query Match      25.2%; Score 194; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 2.2e-193;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 RKRVDLEQKMKVVENLQDDFDNFYKTLKSGDMDLNGNQSVTQRKMQQLLEQMLTALD 211
DB 23 rkrvqdeqkmkvvlenlqddfdnfykltksgdmdlgnngsvtrqkmgqleqmltald 82
QY 212 QMRRSIVSELAGLSAMEYVQKTLTDEELADWKRRPEIACIGPPNICLDRLNNWITSIA 271
DB 83 qmrsvselagilameyvqkltldeeadwkrpeiacigppnicldrlenwitsia 142
QY 272 ESOLQTRQOIKKLEELQOKVSKGDPVQHRPMLERIVELFRNLKMSAFVVERQPCMPM 331
DB 143 esqltrqrqkllleelqkvskgdpvqhrpmlerivelfnlmksafvverqpcmpm 202
QY 332 HPDRPLVKTGVQF 345
DB 203 hpdprlviktgvqf 216

RESULT 20
AAY72855
ID AAY72855 standard; protein; 185 AA.
XX
AC AAY72855;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #13 (193-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
XX Mus musculus.
XX
XX Key
XX Region 150..166
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US23822.
XX
```

```
PR 31-AUG-1999; 99US-0387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein -
XX
XX Claim 65; Page: 80; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 193-377
XX amino acids of Stat3 protein.
XX The invention relates to methods for identifying interacting regions of
XX transcription factors and methods for identifying agents which modulates
XX the interaction between a transcription factor such as c-Jun and a Stat
XX protein such as Stat-1 and Stat-3, useful for modulating gene
XX transcription e.g., cellular transformative diseases and also for treating
XX used in the treatment of dysproliferative diseases and also for treating
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
XX transactivation domain.
XX
XX Sequence 185 AA;

Query Match 24.0%; Score 185; DB 22; Length 185;
Best Local Similarity 100.0%; Pred. No. 4.4e-184;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 QSVTRQKMOOLEQMLTALDOMRRSIYSELAGLSAMEYVQKTLTDEELADWKRRIACI 252
DB 1 qsvtrqkmlqleqmtaldqmrriivselagllsameyvqktltdeeladwkrriaci 60

QY 253 GPPNCLDRLENNWITSLAESQLOTRQOIKKLEELQKVSYGDPVQHRPMLERIVEL 312
DB 61 gppncldrleennwitslaesqltrqoikkleelqkvsygdvpvqhrpml eerivel 120

QY 313 FRNLKMSAFVVERQPCMPHDPRLVITKGVQFTTKVRLVLVKEPELNYQLIKVCIDKDS 372
DB 121 frnlkmsafvverqpcmp hdp rlvitkgvqfttkvrlvlvkepelnyqlikvcidkds 180

QY 373 GDVAA 377
DB 181 gdvaa 185

RESULT 21
AAY72848
ID AAY72848 standard; protein; 176 AA.
XX
XX AAY72848;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #6 (107-282 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 24...48
XX /note= "Stat3-c-Jun interaction region 1;
XX corresponds to 130-154 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
```

```
XX
XX 30-AUG-2000; 2000WO-US23822.
XX
XX 31-AUG-1999; 99US-0387418.
XX
XX (UYRQ ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
XX transcription factor c-Jun and a Stat3 protein -
XX
XX Claim 65; Page 74-75; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-282
XX amino acids of Stat3 protein.
XX The invention relates to methods for identifying interacting regions of
XX transcription factors and methods for identifying agents which modulates
XX the interaction between a transcription factor such as c-Jun and a Stat
XX protein such as Stat-1 and Stat-3, useful for modulating gene
XX transcription e.g., cellular transformative diseases and also for treating
XX used in the treatment of dysproliferative diseases and also for treating
XX cancer and psoriasis. A Stat protein comprises the N-terminal domain,
XX coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
XX transactivation domain.
XX
XX Sequence 176 AA;

Query Match 22.9%; Score 176; DB 22; Length 176;
Best Local Similarity 100.0%; Pred. No. 9.9e-175;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 RCLWERSRLQTAATAAQQGQANHPATAVVTQKQOMLEQHLQDVKRVRQDLQKMKVVE 166
DB 1 rclweersrllqtaataaqqgqanhpataavvtqkqomleqhlqdvkrvrqdl eqkmkvv e 60

QY 167 NLQDDFFI NYKTLKSGQDMQDLNGNQSVTROKMOOLEQMLTALDOMRRSIYSELAGLILS 226
DB 61 nlqddfdfykltksqgdmqdlngnnqsvtrqkmgqleqmltaldqmrriivselagil s 120

QY 227 AMEYVQKTLTDEELADWKRRIACIIGGPPNICLDRLENWITSLAESQLOTRQOIK 282
DB 121 ameyvqktltdeeladwkrriaci iggppnicldr lenwitslaesqltrqqik 176

RESULT 22
AAY72840
ID AAY72840 standard; protein; 154 AA.
XX
XX AAY72840;
XX
XX 31-MAY-2001 (first entry)
XX
XX Mouse Stat3 protein fragment #1 (1-154 amino acids).
XX
XX Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
XX cellular transformation; dysproliferative disease; cancer; psoriasis;
XX therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Domain 1..130
XX /note= "N-terminal domain"
XX Region 130..154
XX /note= "Stat3-c-Jun interaction region 1"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
```

XX 30-AUG-2000; 2000WO-US23822.
PF
XX 31-AUG-1999; 99US-0387418.
PR
XX (UYRQ) UNIV ROCKEFELLER.
PA
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI WPI; 2001-226705/23.
XX
DR
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
PT
XX
PS Claim 65; Page 66-67; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 1-154
CC amino acids of Stat3 protein. This Stat3 fragment showed very weak
CC binding to c-Jun protein in the cell extract.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3 useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX
SQ Sequence 154 AA;

Query Match 20.0%; Score 154; DB 22; Length 154;
Best Local Similarity 100.0%; Pred. No. 7.2e-152;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNLQQLDTRYLKHOLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 maqwnqlqldtrylkhlqlysdtfpmlrqlflapwiesqdwyaaskeshatlvfhn 60
QY 61 LGEIDQOQYSRFLQESNVLYQHNRIRIKQFLQSRYLKPMELRIARIVARCLWEESRLIQATA 120
DB 61 lgeidqoqysrflqesnvlyqhnirrikqflqsrylekpmelriarivarclweesrllqtaa 120
QY 121 TAAQGGQGANHPTAAVYTEKQOMLEQHLQDVKRK 154
DB 121 taaqggganhptaavvtekqgmleqhlqdvkrk 154

RESULT 23
AAY72849
ID AAY72849 standard; protein; 143 AA.
XX
AC AAY72849;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #7 (107-249 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 24..48
FT /note= "Stat3-c-Jun interaction region 1;
FT corresponds to 130-154 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US23822.
PF
XX 31-AUG-1999; 99US-0387418.
PR
XX (UYRQ) UNIV ROCKEFELLER.
PA
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
PI WPI; 2001-226705/23.
XX
DR
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
PT
XX
PS Claim 65; Page 75-76; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 107-249
CC amino acids of Stat3 protein.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX
SQ Sequence 143 AA;

Query Match 18.6%; Score 143; DB 22; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.9e-140;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 RCLWEESRLQLQTAATAAQGGQGANHPTAAVYTEKQOMLEQHLQDVYRKVRQDLQKMKVVE 166
DB 1 rclweesrlqlqtaataaqqggganhptaavvtekqgmleqhlqdvkrvqdlqkmkvve 60
QY 167 NLQODFDFPNYKTLKSGQMDLNGNNSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLS 226
DB 61 nlqddfdfnkylksqgdmqldngnnsvtrqkmooleqmltaldomrrsivselaglls 120
QY 227 AMEYVOKTLTDEELADWKRPEI 249
DB 121 ameyvoktltdeeladwkrpei 143

RESULT 24
AAY07240
ID AAY07240 standard; Protein; 141 AA.
XX
AC AAY07240;
XX
DT 06-JUL-1999 (first entry)
XX
DE Fragment of human hepatic STAT3 protein.
XX
KW Placenta; isoform; human; STAT3; intracellular; transcription factor;
KW Signal Transducer and Activator of Transcription; allele; growth arrest;
KW hepatic acute-phase protein; monocytic cell; myeloma; autoimmune disease;
KW inflammation.
XX
OS Homo sapiens.
XX
PN EP906953-A1.
XX
PD 07-APR-1999.
XX
PF 16-SEP-1997; 97EP-0116061.
XX
PR 16-SEP-1997; 97EP-0116061.
XX

PA	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.	XX	Claim 8; Column 99-102; 206pp; English.
XX		PS	
PI	Della Pietra L, Serlupi-Crescenzi O;	XX	The present sequence is that of the DNA binding domain of human
XX		CC	signal transducer and activator of transcription 3 (STAT-3), i.e.
XX		CC	amino acids 321-493 of the full-length protein (see AAB19964). The
DR	WPI; 1999-207107/18.	CC	domain includes an immunoglobulin-type fold. The invention provides
DR	N-PSDB; AAX29976.	CC	a crystal of a core portion of a STAT protein in dimer form with an
XX		CC	18-mer duplex DNA (see AAA89233) that contains a binding site for
PT	New allelic variant of human STAT3 useful in treating autoimmune or	CC	the STAT dimer. The core portion comprises a coiled-coil domain,
PT	inflammatory diseases	CC	the DNA binding domain, a SH2 domain and a linker domain that joins
XX		CC	the DNA binding and SH2 domains. The crystal is of sufficient
PS	Claim 2; Page 10-11; 22pp; English.	CC	quality to perform x-ray crystallography studies. Methods of
XX		CC	preparing the crystals are included in the invention. Knowledge of
CC	This sequence represents a fragment of the hepatic allelic isoform	CC	the STAT protein's 3-dimensional structure will aid in
CC	of human Signal Transducer and Activator of Transcription (STAT3)	CC	structure-based drug design. The crystal can be used in drug
CC	intracellular transduction factor (Akira et al., Cell 77, 63-71	CC	screening assays to identify agonist and antagonist compounds.
CC	(1994)). The invention relates to isolation of allelic variants of	CC	Antagonists can be used to treat inflammation, allergy, asthma and
CC	the placental hSTAT3 sequence. hSTAT3 plays a role in the upregulation	CC	leukaemia, and agonists to treat anaemia, neutropenia,
CC	of hepatic acute-phase proteins, growth arrest of monocytic cells and	CC	thrombocytopenia, cancer, obesity, viral diseases, growth
CC	in the survival of myeloma cells and so may be used to treat or diagnose	CC	retardation, and other conditions characterized by insufficient
CC	autoimmune or inflammatory diseases.	CC	STAT activity. Fusion proteins comprising a portion of STAT,
XX		CC	especially the DNA binding domain, and a fusion partner are also
XX		CC	disclosed.
SO	Sequence 141 AA;	XX	Sequence 173 AA;
Query Match 18.3%; Score 141; DB 20; Length 141;			
Best Local Similarity 100.0%; Pred. No. 2.3e-138;			
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	564 WLDNIIDLKYLALWNEGYIMGFISKERERATLTKPPGTFLFRFSSSKGGVTFTW 623	QY	321 FVVEROPCPMPHPDRPLVIKTVQFTTKVRLLVKTPPELVNQLKIKVCIDKSDVAALRG 380
DB	1 wldnidlkvkylalwnegyimgfiskereraistkppgtfllrfsskskggvtftw 60	DB	1 fvverqpcmpmpdrplviktgvqfttkvrlivktpelnyqlkikvcidksgdvaalrg 60
QY	624 VEKDISGKTQIOSVEPYTKQOLNNMSPAEIIMGYKIMDATNILVSPILVLYPDIPKEEAF 683	QY	381 SRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREORCGNGGRANCASLIVTEELHLIT 440
DB	61 vekdisgktqigsvepytkqolnnmsfaeiimgykimdatnilvspilvlypdipkeef 120	DB	61 srkfnilgtntkvmnmeesnngslsaefkhltilreqcnggrancdaslivteeihlit 120
QY	684 GKYCRPESQEHPEADPGSAAP 704	QY	441 FETEVHQGLKIDLETHSL 459
DB	121 gkycrpesqehpeadpgsaap 141	DB	121 fetevyhqqikidlethsl 139
RESULT 25			
AAB19973		RESULT 26	
ID	AAB19973 standard; Protein; 173 AA.	AAI07241	
XX		ID	AAI07241 standard; Protein; 141 AA.
AC	AAB19973;	XX	
XX		XX	AAI07241;
DT	28-MAR-2001 (first entry)	DT	06-JUL-1999 (first entry)
XX		XX	
DE	Human STAT-3 DNA binding domain.	DE	Fragment of mouse hepatic STAT3 protein.
XX		XX	
KW	STAT-3; signal transducer and activator of transcription 3;	KW	Placenta; isoform; human; STAT3; intracellular; transcription factor;
KW	human; crystal; drug screening; DNA binding domain.	KW	Signal Transducer and Activator of Transcription; allele; growth arrest;
OS	Homo sapiens.	KW	hepatic acute-phase protein; monocytic cell; myeloma; autoimmune disease;
XX		XX	inflammation.
XX	US6160092-A.	XX	
XX	12-DEC-2000.	XX	Mus sp.
XX		OS	
PF	29-MAY-1998; 98US-0087465.	XX	
XX		XX	EP906953-Al.
PR	29-MAY-1998; 98US-0087465.	XX	
XX		XX	07-APR-1999.
PA	(UYRQ) UNIV ROCKEFELLER.	XX	
XX		XX	16-SEP-1997; 97EP-0116061.
PI	Chen X, Darnell JE, Kuriyan J, Vinkemeier U, Zhao Y, Jeruzalmi D;	XX	
XX		XX	16-SEP-1997; 97EP-0116061.
DR	WPI; 2001-101568/11.	XX	(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
DR	N-PSDB; AAA89239.	XX	Della Pietra L, Serlupi-Crescenzi O;
XX		PI	
PT	Novel crystal useful in drug screening assays, comprises portion of		
PT	signal transducer, activator of transcription and duplex DNA		

XX WPI; 1999-207107/18.
DR N-PSDB; AAX29977.
XX
XX New allelic variant of human STAT3 useful in treating autoimmune or
PT inflammatory diseases
PS
XX
XX Disclosure; Page 12-13; 22pp; English.
XX
XX This sequence represents a fragment of the hepatic allelic isoform
CC of mouse Signal Transducer and Activator of Transcription (STAT3)
CC intracellular transcription factor (Akira et al., Cell 77, 63-71
CC (1994)). The invention relates to isolation of allelic variants of
CC the placental human STAT3 sequence. hSTAT3 plays a role in the
CC upregulation of hepatic acute-phase proteins, growth arrest of monocytic
CC cells and in the survival of myeloma cells and so may be used to treat
CC or diagnose autoimmune or inflammatory diseases.
XX
SQ Sequence 141 AA;

Query Match 17.9%; Score 138; DB 20; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.1e-135; Length 141;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 564 WLDNIIDLKYYIALWNEGYIMGFISKERERAILSTKPGTFLFRFSSKGGVFTTW 623
Db 1 wldniidlkvkyyialwnegyimgfiskerailstckpgtflfrfssksggvftfw 60

Qy 624 VEKDISGKTQIQSVPTKQOLNNMSFAEIIIMGYKINDATNIIIVSLVLYLPDIPKEAF 683
Db 61 vekdisgktqiqsvptkqolnnmsfaeiiimgykindatniiivslvlylpdipkeaf 120

Qy 684 GKYCRPESQEHPEADPGS 701
Db 121 gkycrpesqehpeadpgs 138

RESULT 27
AAY72856
ID AAY72856 standard; protein; 129 AA.
XX
AC AAY72856;
XX
XX 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #14 (249-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 94..110
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US23822.
XX
XX 31-AUG-1999; 99US-0387418.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX

PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
XX
PS Claim 65; Page 80-81; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 249-377
CC amino acids of Stat3 protein.
CC The invention relates to methods for identifying interacting regions of
CC transcription factors and methods for identifying agents which modulates
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX
SQ Sequence 129 AA;

Query Match 16.8%; Score 129; DB 22; Length 129;
Best Local Similarity 100.0%; Pred. No. 6.7e-126;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 IACIGPPNICLDRLNWTSLAESQLOTRQOIKKLEELQOKVSKGDPVOHRPMLER 308
Db 1 iacigppnicldrlenwtslaesqltrqkikleeiqkvskgdpivqhrpmler 60

Qy 309 IVELFNLMKSAFVERQPCMPMPDRPLVKTGVQFTTKVRLILVKFPEINTQIKIKVCI 368
Db 61 ivelfnmlksafverqpcmpmpdrplviktgvqfttkvrlilvkfpeintqikikvci 120

Qy 369 DKDSGDVAA 377
Db 121 dkdsgdvaa 129

RESULT 28
AAY72852
ID AAY72852 standard; protein; 128 AA.
XX
AC AAY72852;
XX
XX 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #10 (155-282 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
XX WO200116605-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US23822.
XX
XX 31-AUG-1999; 99US-0387418.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
XX Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
XX
XX Claim 65; Page 78; 86pp; English.
XX
XX The present sequence is mouse Stat3 protein fragment containing 155-282
XX


```
Query Match      13.4%; Score 103; DB 20; Length 141;
Best Local Similarity 100.0%; Pred. No. 8.7e-99;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 564 WLDNIIDLVKYILALWNEGVIKSKERERAILSTKPPGTFLRLRFSSESKGGVFTTW 623
DB 1 WLDNIIDLVKYILALWNEGVIKSKERERAILSTKPPGTFLRLRFSSESKGGVFTW 60

QY 624 VEKDISGKTQISQVETPKQOLNNMSFAEIIIMGYKIMDATNIL 666
DB 61 VEKDISGKTQISQVETPKQOLNNMSFAEIIIMGYKIMDATNIL 103

RESULT 31
AAY72857
ID AAY72857 standard; protein: 96 AA.
XX
AC AAY72857;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #15 (282-377 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FN Key Location/Qualifiers
FT Region 61..77
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US23822.
XX
PR 31-AUG-1999; 99US-0387418.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
XX
PS Claim 65; Page 81; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 282-377
CC amino acids of Stat3 protein.
CC The invention relates to methods for identifying interacting regions of
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX
SQ Sequence 96 AA;

Query Match      12.5%; Score 96; DB 22; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.2e-91;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 KLEELQKQVSKGDPITVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 341
```

```
DB 1 KLEELQKQVSKGDPITVQHRPMLERIVELFNLKMSAFVVERQPCMPMPHDPRLVIKT 60

QY 342 GVQFTTKVRLLVKFPPELNYOLKIKVCIDKDSGDVAA 377
DB 61 GVQFTTKVRLLVKFPPELNYOLKIKVCIDKDSGDVAA 96

RESULT 32
AAY72853
ID AAY72853 standard; protein: 95 AA.
XX
AC AAY72853;
XX
DT 31-MAY-2001 (first entry)
XX
DE Mouse Stat3 protein fragment #11 (155-249 amino acids).
XX
KW Mouse; Stat3 protein; transcription factor; c-Jun; gene transcription;
KW cellular transformation; dysproliferative disease; cancer; psoriasis;
KW therapy.
XX
OS Mus musculus.
XX
FN Key Location/Qualifiers
FT Region 61..77
FT /note= "Stat3-c-Jun interaction region 2;
FT corresponds to 342-358 position of Stat3 protein"
XX
PN WO200116605-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US23822.
XX
PR 31-AUG-1999; 99US-0387418.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI Zhang X, Horvath C, Wrzeszczynska MH, Darnell JE;
XX WPI; 2001-226705/23.
XX
PT Identifying an agent for use in modulating the interaction between
PT transcription factor c-Jun and a Stat3 protein -
XX
PS Claim 65; Page 78; 86pp; English.
XX
CC The present sequence is mouse Stat3 protein fragment containing 155-249
CC amino acids of Stat3 protein.
CC The invention relates to methods for identifying interacting regions of
CC the interaction between a transcription factor such as c-Jun and a Stat
CC protein such as Stat-1 and Stat-3, useful for modulating gene
CC transcription e.g., cellular transformation. These identifying agents are
CC used in the treatment of dysproliferative diseases and also for treating
CC cancer and psoriasis. A Stat protein comprises the N-terminal domain,
CC coiled-coil domain, DNA binding domain, linker domain, SH2 domain and
CC transactivation domain.
XX
SQ Sequence 95 AA;

Query Match      12.3%; Score 95; DB 22; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.3e-90;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 VQDLEQKMKVVENLQDDFDNFYKTLKSGDMDLNGNNSVTROKMQOLEQMLTALDQMR 214
DB 1 VQDLEQKMKVVENLQDDFDNFYKTLKSGDMDLNGNNSVTROKMQOLEQMLTALDQMR 60

QY 215 RSIVSELAGLLSAMEYVOKTLTDEELADWKRPEI 249
DB 61 RSIVSELAGLLSAMEYVQKTLTDEELADWKRPEI 95

Search completed: March 20, 2002, 08:46:10
```

us-08-212-185-12.olig.rag

Wed Mar 20 11:17:36 2002

Job time: 242 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2002, 08:42:28 ; Search time 64.76 seconds
(without alignments)
267.565 Million cell updates/sec

Title: US-08-212-185-12
Perfect score: 770
Sequence: 1 MAOWNQLQDTRYLKQLHQ.....QFESLTFMDLTSECATSPM 770

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	100.0	770	1	US-08-369-796-12
2	770	100.0	770	2	US-08-852-091-12
3	770	100.0	770	2	US-08-820-754-12
4	770	100.0	770	3	US-08-956-652-12
5	770	100.0	770	3	US-08-956-869-12
6	770	100.0	770	4	US-08-948-547-12
7	770	100.0	770	4	US-09-364-970-3
8	770	100.0	770	5	PCT-US95-17025-12
9	661	85.8	770	4	US-09-364-970-5
10	568	73.8	770	3	US-09-012-710-8
11	442	57.4	770	1	US-08-416-581B-9
12	221	28.7	770	1	US-08-416-581B-1
13	221	28.7	770	1	US-08-416-581B-5
14	221	28.7	770	4	US-09-087-465-6
15	221	28.7	771	1	US-08-276-099A-14
16	221	28.7	771	1	US-08-781-890-14
17	139	18.1	173	4	US-09-087-465-26
18	112	14.5	112	1	US-08-369-796-14
19	112	14.5	112	2	US-08-852-091-14
20	112	14.5	112	5	PCT-US95-17025-14
21	12	1.6	107	4	US-09-087-465-22
22	12	1.6	712	1	US-08-369-796-6
23	12	1.6	712	2	US-08-852-091-6
24	12	1.6	712	2	US-08-820-754-6
25	12	1.6	712	3	US-08-956-652-6
26	12	1.6	712	3	US-08-956-869-6
27	12	1.6	712	3	US-08-948-547-6

28	12	1.6	712	5	PCT-US95-17025-6	Sequence 6, Appl
29	12	1.6	740	1	US-08-276-099A-12	Sequence 12, Appl
30	12	1.6	740	1	US-08-781-890-12	Sequence 12, Appl
31	12	1.6	749	1	US-08-369-796-8	Sequence 8, Appl
32	12	1.6	749	2	US-08-852-091-8	Sequence 8, Appl
33	12	1.6	749	2	US-08-820-754-8	Sequence 8, Appl
34	12	1.6	749	3	US-08-956-652-8	Sequence 8, Appl
35	12	1.6	749	3	US-08-956-869-8	Sequence 8, Appl
36	12	1.6	749	3	US-09-012-710-7	Sequence 7, Appl
37	12	1.6	749	3	US-08-948-547-8	Sequence 8, Appl
38	12	1.6	749	5	PCT-US95-17025-8	Sequence 8, Appl
39	12	1.6	750	1	US-08-369-796-4	Sequence 4, Appl
40	12	1.6	750	2	US-08-852-091-4	Sequence 4, Appl
41	12	1.6	750	2	US-08-820-754-4	Sequence 4, Appl
42	12	1.6	750	3	US-08-956-652-4	Sequence 4, Appl
43	12	1.6	750	3	US-08-956-869-4	Sequence 4, Appl
44	12	1.6	750	3	US-08-948-547-4	Sequence 4, Appl
45	12	1.6	750	4	US-09-087-465-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-369-796-12
; Sequence 12, Application US/08369796
; Patent No. 5716622
; GENERAL INFORMATION:
; APPLICANT: James E. Darnell, Jr.
; APPLICANT: Zilong Wen
; APPLICANT: Curt M. Horvath
; APPLICANT: Zhong Zhong
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/369,796
; FILING DATE: 06-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-369-796-12

Query Match 100.0%; Score 770; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOWNQLQDTRYLKQLHQLYSDTFPMELROFLAPWIESQDWAYAAKESHATLVFHNH 60

Db 601 KPGCTELLRFSESSKEGGVTFTWVEKDLSGKTQIQSVPEYTKQQLNNMSFAEIMGYKIM 660
Qy 661 DATNILVSPVLVLYPDIPKEAEFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720
Db 661 DATNILVSPVLVLYPDIPKEAEFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720
Qy 721 TIDLPMSPRTLDSLMQFGNNGEAGPSAGGQFESLTFDMDLTSECATSPM 770
Db 721 TIDLPMSPRTLDSLMQFGNNGEAGPSAGGQFESLTFDMDLTSECATSPM 770

RESULT 3
US-08-820-754-12
: Sequence 12, Application US/08820754
: Patent No. 5976835
: GENERAL INFORMATION:
: APPLICANT: Darnell Jr., James E.
: APPLICANT: Schindler, Christian W.
: APPLICANT: Fu, Xian-Yuan
: APPLICANT: Wen, Zilong
: APPLICANT: Zhong, Zhong
: TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Klauber & Jackson
: STREET: 411 Hackensack Avenue
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601

COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/820,754
: FILING DATE: 19-MAR-1997
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/212,185
: FILING DATE: 11-MAR-1994
: APPLICATION NUMBER: US 07/980,498
: FILING DATE: 23-NOV-1992

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/854,296
: FILING DATE: 19-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO US93/02569
: FILING DATE: 19-MAR-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/126,588
: FILING DATE: 24-SEP-1993

: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 600-1-073 CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201 487-5800
: TELEFAX: 201 343-1684
: TELEX: 133521
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 770 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-820-754-12

Query Match 100.0%; Score 770; DB 2: Length 770;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAQWNOLOOLDTRYILKOLHOLYSDTFPMELROFLAPWIESODWAYAASKESHATLVFHNH 60
Db 1 MAQWNOLOOLDTRYILKOLHOLYSDTFPMELROFLAPWIESODWAYAASKESHATLVFHNH 60
Qy 61 LGEIDQOYSRFLQESNVLYQHNLRIKOFLOSRYLEKPMETARIIVARCLWESRLQATAA 120
Db 61 LGEIDQOYSRFLQESNVLYQHNLRIKOFLOSRYLEKPMETARIIVARCLWESRLQATAA 120
Qy 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRKRVQDLEOKMKVVENLQDDDFNYKTLK 180
Db 121 TAAQGGQGANHPTAAVTEKQOMLEQHLQDVVRKRVQDLEOKMKVVENLQDDDFNYKTLK 180
Qy 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVOKTLTDEEL 240
Db 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDOMRRSIVSELAGLISAMEYVOKTLTDEEL 240
Qy 241 ADMKRPEIACIGGPNICLDRENNWITSLAESQLOTRQOIKKLEELOKVSYKGDPIVQ 300
Db 241 ADMKRPEIACIGGPNICLDRENNWITSLAESQLOTRQOIKKLEELOKVSYKGDPIVQ 300
Qy 301 HRPMLEERIVELFRNLMSAFVVEROPCPMPHDPRLVTKTGVQFTTKVRLLVKPELNY 360
Db 301 HRPMLEERIVELFRNLMSAFVVEROPCPMPHDPRLVTKTGVQFTTKVRLLVKPELNY 360
Qy 361 OLKIKYCIDKDSGVAALRGSRKFNTLTNTKVMNNEESNNGSLSAEFPKHLTLREORCN 420
Db 361 OLKIKYCIDKDSGVAALRGSRKFNTLTNTKVMNNEESNNGSLSAEFPKHLTLREORCN 420
Qy 421 GGRANDASLIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILY 480
Db 421 GGRANDASLIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILY 480
Qy 481 NMLTNNPKNVNFTKPIGTWQOVAEVLWSQFSSTTKRGLSTROLTTLAELKLLGPGVNTS 540
Db 481 NMLTNNPKNVNFTKPIGTWQOVAEVLWSQFSSTTKRGLSTROLTTLAELKLLGPGVNTS 540
Qy 541 GCOTITWAKFCCKENMAGKGFVWVWLDNIIDLKVKYIALWNEGYIMCFISKERAILST 600
Db 541 GCOTITWAKFCCKENMAGKGFVWVWLDNIIDLKVKYIALWNEGYIMCFISKERAILST 600
Qy 601 KPGCTELLRFSESSKEGGVTFTWVEKDLSGKTQIQSVPEYTKQQLNNMSFAEIMGYKIM 660
Db 601 KPGCTELLRFSESSKEGGVTFTWVEKDLSGKTQIQSVPEYTKQQLNNMSFAEIMGYKIM 660
Qy 661 DATNILVSPVLVLYPDIPKEAEFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720
Db 661 DATNILVSPVLVLYPDIPKEAEFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSN 720
Qy 721 TIDLPMSPRTLDSLMQFGNNGEAGPSAGGQFESLTFDMDLTSECATSPM 770
Db 721 TIDLPMSPRTLDSLMQFGNNGEAGPSAGGQFESLTFDMDLTSECATSPM 770

RESULT 4
US-08-956-652-12
: Sequence 12, Application US/08956652
: Patent No. 6013475
: GENERAL INFORMATION:
: APPLICANT: Darnell Jr., James E.
: APPLICANT: Schindler, Christian W.
: APPLICANT: Fu, Xian-Yuan
: APPLICANT: Wen, Zilong
: APPLICANT: Zhong, Zhong
: TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Klauber & Jackson
: STREET: 411 Hackensack Avenue
: CITY: Hackensack
: STATE: New Jersey

COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: PatentIn Release #1.0, Version #1.25
FILING DATE: 19-MAR-1992
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
us-08-956-652-12

Query Match 100.0%; Score 770; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWLOQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAQWLOQLDTRYLKQLHQLYSDTFPMELRQFLAPWIESQDWAYAASKESHATLVFHNL 60
QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMETARIVARCLWEESRLQATA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLOSRYLEKPMETARIVARCLWEESRLQATA 120
QY 121 TAAQGGQANHPHTAAVTEKQOMLQOHLDQVYKRVODLEQKMKVYVENLQDDFDNFYKTLK 180
DB 121 TAAQGGQANHPHTAAVTEKQOMLQOHLDQVYKRVODLEQKMKVYVENLQDDFDNFYKTLK 180
QY 181 SGDMQDLNCGNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEEL 240
DB 181 SGDMQDLNCGNQSVTRQKMOQLEQMLTALDQMRRSIVSELAGLSAMEYVQKTLTDEEL 240
QY 241 ADWKRPEIACIGGPNICLDRENLWITSLSAESQLOTRQOIKKLELOOKVSYKGDPIVQ 300
DB 241 ADWKRPEIACIGGPNICLDRENLWITSLSAESQLOTRQOIKKLELOOKVSYKGDPIVQ 300
QY 301 HRPMLEERIVELFRNLMSAFVYVQPCMPMPHDPRLVTKTGQVFTTKVRLLVKPELNY 360
DB 301 HRPMLEERIVELFRNLMSAFVYVQPCMPMPHDPRLVTKTGQVFTTKVRLLVKPELNY 360
QY 361 QLKIKVICDKSDVAALRGSRKFNILGTNTKVMNNEESNGLSAPFKHLTLRQRCGN 420
DB 361 QLKIKVICDKSDVAALRGSRKFNILGTNTKVMNNEESNGLSAPFKHLTLRQRCGN 420

QY 421 GGRANDASLIIVTEELHLLITETEVYHOGKIDLETHSLPVVVISNICOMPANASILWY 480
DB 421 GGRANDASLIIVTEELHLLITETEVYHOGKIDLETHSLPVVVISNICOMPANASILWY 480
QY 481 NMLTNNPKNVNFFTKPIGTWDOVAEVLWSQFSSSTTKRGLSIEQLTTTAEKLLGPGVNY 540
DB 481 NMLTNNPKNVNFFTKPIGTWDOVAEVLWSQFSSSTTKRGLSIEQLTTTAEKLLGPGVNY 540
QY 541 GCOITWAKFCENMAGKGFSPWVWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600
DB 541 GCOITWAKFCENMAGKGFSPWVWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600
QY 601 KPGGTFLFRFSESSKEGGVTFWVEKDISGKTQIOSVEPYTKQQLNNMSFAEIIINGYKIM 660
DB 601 KPGGTFLFRFSESSKEGGVTFWVEKDISGKTQIOSVEPYTKQQLNNMSFAEIIINGYKIM 660
QY 661 DATNLLVSPVLYPDIPKEEAFGKYCRPESOEHPADGSAAPYLKTKFCVTFPTTCSN 720
DB 661 DATNLLVSPVLYPDIPKEEAFGKYCRPESOEHPADGSAAPYLKTKFCVTFPTTCSN 720
QY 721 TIDLPMSPRTLDSLMQFGNNGEAPSGAGQFESI.TFDMDLTSECATSPM 770
DB 721 TIDLPMSPRTLDSLMQFGNNGEAPSGAGQFESI.TFDMDLTSECATSPM 770

RESULT 5
US-08-956-869-12
Sequence 12, Application US/08956869
Patent No. 6030808
GENERAL INFORMATION:
APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/212,185
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-956-869-12

Query Match 100.0%; Score 770; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMLROFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMLROFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIIVARCLWESRLLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIIVARCLWESRLLQTAA 120
Qy 121 TAAQOQGOANHPHTAAVVTKEQOMLEQHLQDQVRKRVQDLEQKMKVVENLODDDFNFKTLK 180
Db 121 TAAQOQGOANHPHTAAVVTKEQOMLEQHLQDQVRKRVQDLEQKMKVVENLODDDFNFKTLK 180
Qy 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
Db 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
Qy 241 ADMKRRPEIACIGPPNICDLRENMTSLAESQLQTRQOIKKLEEOQKVSXKGDPIVQ 300
Db 241 ADMKRRPEIACIGPPNICDLRENMTSLAESQLQTRQOIKKLEEOQKVSXKGDPIVQ 300
Qy 301 HRPLERIVERLFRNLKMSAFVVEROPCPMPHDPRLVTKTGVQFTTKVRLLVKPELNY 360
Db 301 HRPLERIVERLFRNLKMSAFVVEROPCPMPHDPRLVTKTGVQFTTKVRLLVKPELNY 360
Qy 361 QLKIKVICDKSDGVAALRGSRKFNILGTNTKVMNNEESNNGSLSAEFKHLTLRQRCGN 420
Db 361 QLKIKVICDKSDGVAALRGSRKFNILGTNTKVMNNEESNNGSLSAEFKHLTLRQRCGN 420
Qy 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILMY 480
Db 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILMY 480
Qy 481 NMLTNPKNNVFTKPPIGTWQDQVAVLSWQFSSTTKRGLSIEOLTTLAEKLLGPGVNY 540
Db 481 NMLTNPKNNVFTKPPIGTWQDQVAVLSWQFSSTTKRGLSIEOLTTLAEKLLGPGVNY 540
Qy 541 GCQITWAKFKCKENMACKGFSFWWLDNIIDLKVKYILALWNEGYIMGFISKERAILST 600
Db 541 GCQITWAKFKCKENMACKGFSFWWLDNIIDLKVKYILALWNEGYIMGFISKERAILST 600
Qy 601 KPCTFLLRSESSKGGVFTTWEXDLSGKTQIQSVPEYTKQOLNMMSFAELIMCYKIM 660
Db 601 KPCTFLLRSESSKGGVFTTWEXDLSGKTQIQSVPEYTKQOLNMMSFAELIMCYKIM 660
Qy 661 DATNILVSPVLVYLPDIPKEAFKCYCRPESQHPHADPCSAAPYLUKTKFTICVPTTCSN 720
Db 661 DATNILVSPVLVYLPDIPKEAFKCYCRPESQHPHADPCSAAPYLUKTKFTICVPTTCSN 720
Qy 721 TIDLPHSPRTLDSLMQFGNNGEGAFPSAGQFESLTFDMDLTSECATSPM 770
Db 721 TIDLPHSPRTLDSLMQFGNNGEGAFPSAGQFESLTFDMDLTSECATSPM 770

RESULT 6
US-08-948-547-12
Sequence 12, Application US/08948547
Patent No. 6124118
GENERAL INFORMATION:

APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,547
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/854,296
FILING DATE: 19-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-547-12

Query Match 100.0%; Score 770; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMLROFLAPWIESQDWAYAASKESHATLVFHNL 60
Db 1 MAQWNOLOOLDTRYLKQLHOLYSDTFPMLROFLAPWIESQDWAYAASKESHATLVFHNL 60
Qy 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIIVARCLWESRLLQTAA 120
Db 61 LGEIDQOYSRFLQESNVLYOHNLRRIKQFLOSRYLEKPMETARIIVARCLWESRLLQTAA 120
Qy 121 TAAQOQGOANHPHTAAVVTKEQOMLEQHLQDQVRKRVQDLEQKMKVVENLODDDFNFKTLK 180
Db 121 TAAQOQGOANHPHTAAVVTKEQOMLEQHLQDQVRKRVQDLEQKMKVVENLODDDFNFKTLK 180
Qy 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240
Db 181 SOGDMODLNGNOSVTRQKMOOLEQMLTALDOMRRSIVSELAGLLSAMYVOKTLTDEEL 240

Db 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEEL 240
QY 241 ADWKRPEIACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300
Db 241 ADWKRPEIACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300
QY 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNY 360
Db 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNY 360
QY 361 QLKIKVICDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420
Db 361 QLKIKVICDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420
QY 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILMY 480
Db 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILMY 480
QY 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540
Db 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540
QY 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600
Db 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600
QY 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIM 660
Db 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIM 660
QY 661 DATNILVSPVLYLPDIKPEEAFKGYCRPESQEHPEADPGSAAPYLKTKFICVTPPTCSN 720
Db 661 DATNILVSPVLYLPDIKPEEAFKGYCRPESQEHPEADPGSAAPYLKTKFICVTPPTCSN 720
QY 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770
Db 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770
RESULT 7
US-09-364-970-3
: Sequence 3, Application US/09364970
: Patent No. 6235873
: GENERAL INFORMATION:
: APPLICANT: Bromberg, Jacqueline
: TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
: TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
: TITLE OF INVENTION: DYSPLASIA-INDUCING CELLULAR CHANGES
: FILE REFERENCE: 600-1-252
: CURRENT APPLICATION NUMBER: US/09/364,970
: CURRENT FILING DATE: 1999-07-31
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 770
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-364-970-3
Query Match 100.0%; Score 770; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAONHLOQLDTRYLKOLHQLYSDTFPMELRQFLAPHIESQDWAYAASKESHATLVPHNL 60
Db 1 MAONHLOQLDTRYLKOLHQLYSDTFPMELRQFLAPHIESQDWAYAASKESHATLVPHNL 60
QY 61 LGEIDQOYSRFOESNVLYQHNLRIKQFLOSRYLEKPMETARIVARCLWEESRLQATA 120
Db 61 LGEIDQOYSRFOESNVLYQHNLRIKQFLOSRYLEKPMETARIVARCLWEESRLQATA 120
QY 121 TAAOQGOANHPTAAVVTETKQMLEQHLQDVRKRVQDLEOKMKVVENLQDDDFNFKTLK 180

Db 121 TAAOQGOANHPTAAVVTETKQMLEQHLQDVRKRVQDLEOKMKVVENLQDDDFNFKTLK 180
QY 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEEL 240
Db 181 SOGDMODLNGNNSVTRQKMOOLEQMLTALDQMRRSIVSELAGLLSAMEYVOKTLTDEEL 240
QY 241 ADWKRPEIACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300
Db 241 ADWKRPEIACIGGPPNCLDRLENWITSLSAESQLOTRQOIKKLEELQOKVSYKGDPIVQ 300
QY 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNY 360
Db 301 HRPMLERIVELFRNLMSAFVVERQPCMPHDPRLVIKTVQFTTKVRLLVKFPPELNY 360
QY 361 QLKIKVICDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420
Db 361 QLKIKVICDKSDGVAALRGSRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGN 420
QY 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILMY 480
Db 421 GGRANDASLIIVTEELHLITFETEVYHOGKIDLETHSLPVVVISNICOMPNAWASILMY 480
QY 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540
Db 481 NMLTNNPKNVNFTKPPITGTDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540
QY 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600
Db 541 GCOITWAKFCKENMAGKGFSPWWLDNIIDLKVKYILALWNEGYIMGFISKERERAILST 600
QY 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIM 660
Db 601 KPPGTFLLRFSSESSKEGGVFTTWVEKDLSGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIM 660
QY 661 DATNILVSPVLYLPDIKPEEAFKGYCRPESQEHPEADPGSAAPYLKTKFICVTPPTCSN 720
Db 661 DATNILVSPVLYLPDIKPEEAFKGYCRPESQEHPEADPGSAAPYLKTKFICVTPPTCSN 720
QY 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770
Db 721 TIDLPMSPRTLDSLMQFGNNGEAGPESAGGQFESLTFDMDLTSECATSPM 770
RESULT 8
PCT-US95-17025-12
: Sequence 12, Application PC/TUS9517025
: GENERAL INFORMATION:
: APPLICANT: James E. Darnell, Jr.
: APPLICANT: Zilong Wen
: APPLICANT: Curt M. Horvath
: APPLICANT: Zhong Zhong
: TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
: TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
: NUMBER OF SEQUENCES: 39
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Klauber & Jackson
: STREET: 411 Hackensack Avenue
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/17025
: FILING DATE: 28-DEC-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/369,796

;; FILING DATE: 06-JAN-1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jackson Esq., David A.
;; REGISTRATION NUMBER: 26,742
;; REFERENCE/DOCKET NUMBER: 600-1-116
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201 487-5800
;; TELEFAX: 201 343-1684
;; TELEX: 133521
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 770 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-17025-12

Query Match 100.0%; Score 770; DB 5; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQGANHPTAAVYTEKQOQMLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 180
DB 121 TAAQGGQGANHPTAAVYTEKQOQMLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 180

QY 181 SQGDMODLNGNQSVTRQKMOQLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 240
DB 181 SQGDMODLNGNQSVTRQKMOQLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 240

QY 241 ADWKRPEIACIGGPNICLDRLNNWITSLAESOLQTRQOIKKLEELQOQVSKYKGDPIVQ 300
DB 241 ADWKRPEIACIGGPNICLDRLNNWITSLAESOLQTRQOIKKLEELQOQVSKYKGDPIVQ 300

QY 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLPLVIKTGVQFTTKVRLLVKFPPELNY 360
DB 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLPLVIKTGVQFTTKVRLLVKFPPELNY 360

QY 361 OLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLLTLRQRCGN 420
DB 361 OLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLLTLRQRCGN 420

QY 421 GGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVVVVISNICOMPNAWASILWY 480
DB 421 GGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVVVVISNICOMPNAWASILWY 480

QY 481 NMLTNPKNVNFFTKPPIGTWDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540
DB 481 NMLTNPKNVNFFTKPPIGTWDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540

QY 541 GCQITWAKFCENMAGKGSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600
DB 541 GCQITWAKFCENMAGKGSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600

QY 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIQSVEPYTKQOLNNMSFAEIMGYKIM 660
DB 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIQSVEPYTKQOLNNMSFAEIMGYKIM 660

QY 661 DATNILVPLVLYLVDIPKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVPTTCSN 720
DB 661 DATNILVPLVLYLVDIPKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVPTTCSN 720

QY 721 TIDLPMSPRTLDSLMQFNGNGEAGPSAGQGFESLTFDMDLTSECATSPM 770
DB 721 TIDLPMSPRTLDSLMQFNGNGEAGPSAGQGFESLTFDMDLTSECATSPM 770

Db 721 TIDLPMSPRTLDSLMQFNGNGEAGPSAGQGFESLTFDMDLTSECATSPM 770

RESULT 9
US-09-364-970-5
; Sequence 5, Application US/09364970
; Patent No. 6235873
; GENERAL INFORMATION:
; APPLICANT: Bromberg, Jacqueline
; TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
; TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
; TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES
; FILE REFERENCE: 600-1-252
; CURRENT APPLICATION NUMBER: US/09/364,970
; CURRENT FILING DATE: 1999-07-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PATVIEW Ver. 2.0
; SEQ ID NO 5
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5

Query Match 85.8%; Score 661; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60
DB 1 MAQWNOLOQLDTRYLKQLHQLYSDFPMELOFLAPWIESQDWAYAASKESHATLVFHNL 60

QY 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120
DB 61 LGEIDQOYSRFLQESNVLYQHNLRIKQFLQSRYLEKPMELIARIVARCLWEESRLQTAA 120

QY 121 TAAQGGQGANHPTAAVYTEKQOQMLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 180
DB 121 TAAQGGQGANHPTAAVYTEKQOQMLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 180

QY 181 SQGDMODLNGNQSVTRQKMOQLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 240
DB 181 SQGDMODLNGNQSVTRQKMOQLEQHLQDVVRKRVODLEQKMKVVENLODDDFENYKTLK 240

QY 241 ADWKRPEIACIGGPNICLDRLNNWITSLAESOLQTRQOIKKLEELQOQVSKYKGDPIVQ 300
DB 241 ADWKRPEIACIGGPNICLDRLNNWITSLAESOLQTRQOIKKLEELQOQVSKYKGDPIVQ 300

QY 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLPLVIKTGVQFTTKVRLLVKFPPELNY 360
DB 301 HRPMLEERIVELFRNLKMSAFVVERQPCMPHDPRLPLVIKTGVQFTTKVRLLVKFPPELNY 360

QY 361 OLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLLTLRQRCGN 420
DB 361 OLKIKVCIDKSDGVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLLTLRQRCGN 420

QY 421 GGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVVVVISNICOMPNAWASILWY 480
DB 421 GGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVVVVISNICOMPNAWASILWY 480

QY 481 NMLTNPKNVNFFTKPPIGTWDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540
DB 481 NMLTNPKNVNFFTKPPIGTWDQVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNY 540

QY 541 GCQITWAKFCENMAGKGSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600
DB 541 GCQITWAKFCENMAGKGSFWWLDNIIDLVKKYILALWNEGYIMGFISKERERAILST 600

QY 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIQSVEPYTKQOLNNMSFAEIMGYKIM 660
DB 601 KPGTFTLLRFSSESSKEGGVFTTWVEKDISGKTQIQSVEPYTKQOLNNMSFAEIMGYKIM 660

QY 661 DATNILVPLVLYLVDIPKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVPTTCSN 720
DB 661 DATNILVPLVLYLVDIPKEEAFGKYCRPESQHPADPGSAAPYLKTKFICVPTTCSN 720

QY 721 TIDLPMSPRTLDSLMQFNGNGEAGPSAGQGFESLTFDMDLTSECATSPM 770
DB 721 TIDLPMSPRTLDSLMQFNGNGEAGPSAGQGFESLTFDMDLTSECATSPM 770


```

;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-416-581B-9

Query Match      57.4%; Score 442; DB 1; Length 770;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 742; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLR 85
Db 26 FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLR 85
QY 86 IKQFLQSRYLEKPMETARIVARCLWEESRLLQTAATAAOGGQOANHPTAAVVTQKQMLE 145
Db 86 IKQFLQSRYLEKPMETARIVARCLWEESRLLQTAATAAOGGQOANHPTAAVVTQKQMLE 145
QY 146 QHLQDVRRKRVQDLEOKMKVVENLQDDDFNYKTLKSGQDMQDLNGNQSVTRQKMQQLEQ 205
Db 146 QHLQDVRRKRVQDLEOKMKVVENLQDDDFNYKTLKSGQDMQDLNGNQSVTRQKMQQLEQ 205
QY 206 MLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLN 265
Db 206 MLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRPEIACIGGPPNICLDRLN 265
QY 266 WITSLAESOLOTRQOIKKLEELQOQVSKYKGDPIVOHRPMLERIVELFELNLMKSAFVVER 325
Db 266 WITSLAESOLOTRQOIKKLEELQOQVSKYKGDPIVOHRPMLERIVELFELNLMKSAFVVER 325
QY 326 QPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCIDKSDGDAALRGSRKFN 385
Db 326 QPCMPHDPRLPVIKTGVOFTTKVRLLVKPELNYQLKIKVCIDKSDGDAALRGSRKFN 385
QY 386 ILGTNTKYNMMEESNNGSLASBFKHLTLREQRCNGGRANCDAASLIVTEELHLITFETEV 445
Db 386 ILGTNTKYNMMEESNNGSLASBFKHLTLREQRCNGGRANCDAASLIVTEELHLITFETEV 445
QY 446 YHOGKIDLETHSLPVVVISNCOMPNANASILWYNMLTNNPKNPNFTFKPIGTWDOVA 505
Db 446 YHOGKIDLETHSLPVVVISNCOMPNANASILWYNMLTNNPKNPNFTFKPIGTWDOVA 505
QY 506 EVLSWQFSSTTKRGLSIEQLTTLAELKLGPGVNYSCQITWAKFKCKENMAGKGFSEFWWL 565
Db 506 EVLSWQFSSTTKRGLSIEQLTTLAELKLGPGVNYSCQITWAKFKCKENMAGKGFSEFWWL 565
QY 566 DNIIDLKVKYILALWNEGYIMGFISKERERAILSTKPPGTFTLLRFSESSKEGGVFTTWE 625
Db 566 DNIIDLKVKYILALWNEGYIMGFISKERERAILSTKPPGTFTLLRFSESSKEGGVFTTWE 625
QY 626 KDISGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIMDATNILVSPLYLYPDIPKKEAFGK 685
Db 626 KDISGKTQIOSVEPYTKQOLNNMSFAEIIIMGYKIMDATNILVSPLYLYPDIPKKEAFGK 685
QY 686 YCRPESQEHPEADPGSAAPYLTKFCIVTPTTCSNTIDLPMSPTLDSLMOFCNNGEGAE 745
Db 686 YCRPESQEHPEADPGSAAPYLTKFCIVTPTTCSNTIDLPMSPTLDSLMOFCNNGEGAE 745
QY 746 PSAGGOFESLTFDMDLTSECATSPM 770
Db 746 PSAGGOFESLTFDMDLTSECATSPM 770

RESULT 12
US-08-416-581B-1
; Sequence 1, Application US/08416581B
; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadimitsu
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:

```

```

;      ADDRESS: SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET: 2100 Pennsylvania Avenue, N.W.
;      CITY: Washington
;      STATE: D.C.
;      COUNTRY: USA
;      ZIP: 20037
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/416.581B
;      FILING DATE: 04-APR-1995
;      CLASSIFICATION: 435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: JP 6-65825/1994
;      FILING DATE: 04-APR-1994
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Nakamura, Dean H.
;      REGISTRATION NUMBER: 33,981
;      REFERENCE/DOCKET NUMBER: Q-37891
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (202)293-7060
;      TELEFAX: (202)293-7860
;      INFORMATION FOR SEQ ID NO: 1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 770 amino acids
;      TYPE: amino acid
;      STRANDEDNESS:
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-416-581B-1

Query Match      28.7%; Score 221; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3,1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLR 85
Db 26 FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGEIDQOYSRFLQESNVLYQHNLR 85
QY 86 IKQFLQSRYLEKPMETARIVARCLWEESRLLQTAATAAOGGQOANHPTAAVVTQKQMLE 145
Db 86 IKQFLQSRYLEKPMETARIVARCLWEESRLLQTAATAAOGGQOANHPTAAVVTQKQMLE 145
QY 146 QHLQDVRRKRVQDLEOKMKVVENLQDDDFNYKTLKSGQDMQDLNGNQSVTRQKMQQLEQ 205
Db 146 QHLQDVRRKRVQDLEOKMKVVENLQDDDFNYKTLKSGQDMQDLNGNQSVTRQKMQQLEQ 205
QY 206 MLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246
Db 206 MLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246

RESULT 13
US-08-416-581B-5
; Sequence 5, Application US/08416581B
; Patent No. 5719042
; GENERAL INFORMATION:
; APPLICANT: Kishimoto, Tadimitsu
; APPLICANT: Akira, Shizuo
; TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416.581B
; FILING DATE: 04-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-65825/1994
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: O-37891
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 770 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-416-581B-5

Query Match      28.7%; Score 221; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDDOQYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDDOQYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
QY 146 QHLQDVRKRVQDLEOKMKVVENLQDDFDFNYKTLKSGQDMODLNGNNSVTRKMOOLEQ 205
DB 146 QHLQDVRKRVQDLEOKMKVVENLQDDFDFNYKTLKSGQDMODLNGNNSVTRKMOOLEQ 205
QY 206 MLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRR 246
DB 206 MLTALDOMRRSIVSELAGLLSAMEYVOKTLTDEELADWKRR 246

RESULT 15
US-08-276-099A-14
; Sequence 14, Application US/08276099A
; Patent No. 5591825
; GENERAL INFORMATION:
; APPLICANT: McKnight, Steven L
; APPLICANT: Hou, Jinzhao
; TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
; TITLE OF INVENTION: BINDING ASSAYS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276.099A
; FILING DATE: 15-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard Aron
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59451-1/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 398-3249
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-276-099A-14

Query Match      28.7%; Score 221; DB 1; Length 771;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDDOQYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDDOQYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145

Query Match      28.7%; Score 221; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1e-197;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDDOQYSRFLQESNVLYQHNLRR 85
DB 26 FPMELROFLAPWIESODWAYAASKESHATLVFHNLLGEIDDOQYSRFLQESNVLYQHNLRR 85
QY 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145
DB 86 IKQFLOSRYLEKPMETARIVARCLWEESRLLOTAATAAQQGGQOANHPTAAVVTKEOOMLE 145

RESULT 14
US-09-087-465-6
; Sequence 6, Application US/09087465A
; Patent No. 6160092
; GENERAL INFORMATION:
; APPLICANT: Vinkemeier, Uwe
; APPLICANT: Chen, Xiaomin
; APPLICANT: Darnell Jr., James E
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 600-1-229
; CURRENT APPLICATION NUMBER: US/09/087.465A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-087-465-6

```

Db 86 IKQFLQSRYLEKPMPIARIVARCLWEESRLQTAATAAQOQOANHPTAAVTEKQOMLE 145

Qy 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNYKTLKSGQMDLNGNNSVTRKMQOOLEQ 205

Db 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNYKTLKSGQMDLNGNNSVTRKMQOOLEQ 205

Qy 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246

Db 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246

RESULT 16

US-08-781-890-14

: Sequence 14, Application US/08781890

: Patent No. 5710266

: GENERAL INFORMATION:

: APPLICANT: McKnight, Steven L

: APPLICANT: Hou, Jinzhao

: TITLE OF INVENTION: INTERLEUKIN-4 SIGNAL TRANSDUCERS AND

: TITLE OF INVENTION: BINDING ASSAYS

: NUMBER OF SEQUENCES: 17

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: FLEHR, ROHBACH, TEST, ALBRITTON & HERBERT

: STREET: 4 Embarcadero Center, Suite 3400

: CITY: San Francisco

: STATE: California

: COUNTRY: USA

: ZIP: 94111-4187

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/781,890

: FILING DATE: 05-JAN-1997

: CLASSIFICATION: 536

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/276,099

: FILING DATE: 15-JUL-1994

: ATTORNEY/AGENT INFORMATION:

: NAME: Osman, Richard Aron

: REGISTRATION NUMBER: 36,627

: REFERENCE/DOCKET NUMBER: A-59451-1/RAO

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (415) 781-1989

: TELEFAX: (415) 398-3249

: TELEX: 910 277299

: INFORMATION FOR SEQ ID NO: 14:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 771 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

US-08-781-890-14

Query Match 28.7%; Score 221; DB 1; Length 771;

Best Local Similarity 100.0%; Pred. No. 3.1e-197;

Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGELIDQOYSRFLQESNVLYOHNLR 85

Db 26 FPMELRQFLAPWIESQDWAYAASKESHATLVFHNLLGELIDQOYSRFLQESNVLYOHNLR 85

Qy 86 IKQFLQSRYLEKPMPIARIVARCLWEESRLQTAATAAQOQOANHPTAAVTEKQOMLE 145

Db 86 IKQFLQSRYLEKPMPIARIVARCLWEESRLQTAATAAQOQOANHPTAAVTEKQOMLE 145

Qy 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNYKTLKSGQMDLNGNNSVTRKMQOOLEQ 205

Db 146 QHLQDVRRKRVODLEOKMKVVENLQDDDFNYKTLKSGQMDLNGNNSVTRKMQOOLEQ 205

Qy 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246

Db 206 MTLALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRR 246

RESULT 17

US-09-087-465-26

: Sequence 26, Application US/09087465A

: Patent No. 6160092

: GENERAL INFORMATION:

: APPLICANT: Vinkemeier, Uwe

: APPLICANT: Chen, Xiaomin

: APPLICANT: Darnell Jr., James E

: APPLICANT: Kuriyan, John

: TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF

: TITLE OF INVENTION: USE

: FILE REFERENCE: 600-1-229

: CURRENT APPLICATION NUMBER: US/09/087,465A

: CURRENT FILING DATE: 1998-05-29

: NUMBER OF SEQ ID NOS: 37

: SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 26

: LENGTH: 173

: TYPE: PRT

: ORGANISM: Homo sapiens

US-09-087-465-26

Query Match 18.1%; Score 139; DB 4; Length 173;

Best Local Similarity 100.0%; Pred. No. 1.6e-121;

Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 321 FVVERQPCMPHDPRLVIVKTVQFTTKVRLLVKFPPELVQKIKVICDKSDGVAALRG 380

Db 1 FVVERQPCMPHDPRLVIVKTVQFTTKVRLLVKFPPELVQKIKVICDKSDGVAALRG 60

Qy 381 SRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGNGRANCDAASLIVTEELHLIT 440

Db 61 SRKFNLGTNTKVMNMEESNNGSLSAEFKHLTLREORCGNGRANCDAASLIVTEELHLIT 120

Qy 441 FETEVYHQGLKIDLETHSL 459

Db 121 FETEVYHQGLKIDLETHSL 139

RESULT 18

US-08-369-796-14

: Sequence 14, Application US/08369796

: Patent No. 5715622

: GENERAL INFORMATION:

: APPLICANT: James E. Darnell, Jr.

: APPLICANT: Zilong Wen

: APPLICANT: Curt M. Horvath

: APPLICANT: Zhong Zhong

: TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL

: TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS

: NUMBER OF SEQUENCES: 39

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Klauber & Jackson

: STREET: 411 Hackensack Avenue

: CITY: Hackensack

: STATE: New Jersey

: COUNTRY: USA

: ZIP: 07601

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/369,796

: FILING DATE: 06-JAN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-369-796-14

Query Match 14.5%; Score 112; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SLSAEFKHLTLREQRCGNGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVP 462
DB 1 SLSAEFKHLTLREQRCGNGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVP 60

QY 463 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 514
DB 61 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 117

RESULT 19
US-08-852-091-14
Sequence 14, Application US/08852091
Patent No. 5883228
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,091
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
US-08-852-091-14

Query Match 14.5%; Score 112; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 403 SLSAEFKHLTLREQRCGNGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVP 462
DB 1 SLSAEFKHLTLREQRCGNGRANCASLIVTEELHLITFETEVYHOGKIDLETHSLPVP 60

QY 463 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 514
DB 61 VISNICOMPNAWASILWYNMLTNPKNVNFTKPPIGTWDQVAEVLWQFSS 112

RESULT 20
PCT-US95-17025-14
Sequence 14, Application PC/TUS9517025
GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17025
FILING DATE: 28-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal

PCT-US95-17025-14

Query Match 14.5%; Score 112; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 403 SLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHOGKIDLETHSLPVV 462
DB 1 SLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHOGKIDLETHSLPVV 60
QY 463 VISNICOMPNAWASILWYNMLTNNPKNVNFTKPPIGTWDQVAEVLWQFSS 514
DB 61 VISNICOMPNAWASILWYNMLTNNPKNVNFTKPPIGTWDQVAEVLWQFSS 112

Search completed: March 20, 2002, 08:47:27
Job time: 299 sec